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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,759

DATE: 03/01/2002

TIME: 15:00:28

Input Set : A:\terman.txt

Output Set: N:\CRF3\03012002\I870759.raw

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3 <110> APPLICANT: Terman, David S
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
7 <130> FILE REFERENCE: 870759
9 <140> CURRENT APPLICATION NUMBER: US 09/870,759
C--> 10 <141> CURRENT FILING DATE: 2002-01-14
12 <150> PRIOR APPLICATION NUMBER: US 60/208,128
13 <151> PRIOR FILING DATE: 2000-05-30
15 <160> NUMBER OF SEQ ID NOS: 166
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 801
21 <212> TYPE: DNA
22 <213> ORGANISM: Staphylococcus sp.
24 <400> SEQUENCE: 1
25 atgtataaga gattattttat ttcacatgta attttgatat tcgcactgat attagttatt      60
27 tctacaccca acgttttagc agagagtcaa ccagatccta aaccagatga gttgcacaaa      120
29 tcgagtaaat tcaactggttt gatggaaaat atgaaagttt tgtatgatga taatcatgta      180
31 tcagcaataa acgttaaadc tatagatcaa tttctatact ttgacttaat atattctatt      240
33 aaggacacta agttaggga ttatgataat gttcgagtcg aatttaaaaa caaagattta      300
35 gctgataaat acaaagataa atacgtagat gtgtttggag ctaattatta ttatcaatgt      360
37 tatttttcta aaaaaacgaa tgatattaat tcgcatcaaa ctgacaaaacg aaaaacttgt      420
39 atgtatggtg gtgtaactga gcataatgga aaccaattag ataaatatag aagtattact      480
41 gttcgggtat ttgaagatgg taaaaattta ttatcttttg acgtacaaac taataagaaa      540
43 aaggtgactg ctcaagaatt agattaccta actcgtcact atttggtgaa aaataaaaaa      600
45 ctctatgaat ttaacaactc gccttatgaa acgggatata ttaaatttat agaaaatgag      660
47 aatagctttt ggtatgacat gatgcctgca ccaggagata aatttgacca atctaaatat      720
49 ttaatgatgt acaatgacaa taaaatggtt gattctaaag atgtgaagat tgaagtttat      780
51 cttacgacaa agaaaaagtg a                                     801
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 886
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic Sequence
62 <400> SEQUENCE: 2
63 cggctcacag cgcgcccggc tattctcgca ggatcagtcg acatgtataa gagattattt      60
65 atttcacatg taattttgat attcgcactg atattagtta tttctacacc caacgtttta      120
67 gcagagagtc aaccagatcc taaaccagat gagtgcaca aatcgagtaa attcactggt      180
69 ttgatggaaa atatgaaagt tttgtatgat gataatcatg tatcagcaat aaacgttaaa      240
71 tctatagatc aatttctata ctttgactta atatattcta ttaaggacac taagttaggg      300
73 aattatgata atgttcgagt cgaatttaaa aacaaaagatt tagctgataa atacaaaagat      360
75 aaatacgtag atgtgttttg agctaattat tattatcaat gttatttttc taaaaaacg      420
77 aatgatatta attcgcacaa aactgacaaa cgaaaaactt gtatgtatgg tgggtgtaact      480

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79 gagcataatg gaaaccaatt agataaatat agaagtatta ctgttcgggt atttgaagat 540
81 ggtaaaaaatt tattatcttt tgacgtacaa actaataaga aaaagggtgac tgctcaagaa 600
83 ttagattacc taactcgtca ctatttggtg aaaaataaaa aactctatga atttaacaa 660
85 tggccttatg aaacgggata tattaatttt atagaaaatg agaataagctt ttggatgac 720
87 atgatgcctg caccaggaga taaatttgac caatctaaat atttaatgat gtacaatgac 780
89 aataaaaatg ttgattctaa agatgtgaag attgaagttt atcttaacgac aaagaaaaag 840
91 tgaggatcca gacatgataa gataccttga tgagtttggg caaacc 886
94 <210> SEQ ID NO: 3
95 <211> LENGTH: 24
96 <212> TYPE: DNA
97 <213> ORGANISM: Unknown
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Primer
102 <400> SEQUENCE: 3
103 ggcgtcgaca tgtataagag atta 24
106 <210> SEQ ID NO: 4
107 <211> LENGTH: 24
108 <212> TYPE: DNA
109 <213> ORGANISM: Unknown
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Primer
114 <400> SEQUENCE: 4
115 gccggtcct cactttttct ttgt 24
118 <210> SEQ ID NO: 5
119 <211> LENGTH: 22
120 <212> TYPE: DNA
121 <213> ORGANISM: Unknown
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Primer
126 <400> SEQUENCE: 5
127 tatgaaagtt ttgtatgatg at 22
130 <210> SEQ ID NO: 6
131 <211> LENGTH: 20
132 <212> TYPE: DNA
133 <213> ORGANISM: Unknown
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Primer
138 <400> SEQUENCE: 6
139 agtgacgagt taggtaattc 20
142 <210> SEQ ID NO: 7
143 <211> LENGTH: 1443
144 <212> TYPE: DNA
145 <213> ORGANISM: Staphylococcus aureus
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (262)..(1032)
150 <223> OTHER INFORMATION:
153 <400> SEQUENCE: 7
154 ccaaaaataat ggcaagtact ccgttgtcaa taccaagtaa gtaagatatc tgaaatgtat 60

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156 aatagagtaa aaatgaaatc tttttattat attatagaca agtataaaaa aggtatagta 120
158 atatattgat gtataagtaa ataataataa ttctataatt attgtatata actaataatt 180
160 acttcgacaa aaataatcta ttatccaaat atttttagata ataaaaagtt tgtatggaat 240
162 tatgcttttag aggtgagcaa a atg aaa aaa aca gca ttt ata cta ctt tta 291
163 Met Lys Lys Thr Ala Phe Ile Leu Leu Leu
164 1 5 10
166 ttc att gcc cta acg tgg aca aca agt cca ctt gta aat ggt agc gag 339
167 Phe Ile Ala Leu Thr Trp Thr Thr Ser Pro Leu Val Asn Gly Ser Glu
168 15 20 25
170 aaa agc gaa gaa ata aat gaa aaa gat ttg cga aaa aag tct gaa ttg 387
171 Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu
172 30 35 40
174 cag gga gca gct tta ggc aat ctt aaa caa atc tat tat tac aat gaa 435
175 Gln Gly Ala Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu
176 45 50 55
178 aaa gct aaa act gaa aat aaa gag agt cac gat caa ttt tta cag cat 483
179 Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu Gln His
180 60 65 70
182 act ata ttg ttt aaa ggc ttt ttt aca aat cat tca tgg tat aac gat 531
183 Thr Ile Leu Phe Lys Gly Phe Phe Thr Asn His Ser Trp Tyr Asn Asp
184 75 80 85 90
186 tta tta gta gat ttt gat tca aag gat att gtt gat aaa tat aaa ggg 579
187 Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly
188 95 100 105
190 aaa aaa gta gac tta tat ggt gct tat tat ggt tat caa tgt gcg ggt 627
191 Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly
192 110 115 120
194 ggt aca cca aac aaa aca gct tgc atg tat ggt ggt gta acg tta cat 675
195 Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr Leu His
196 125 130 135
198 gat aat aat cga ttg acc gaa gag aaa aaa gtg ccg atc aat tta tgg 723
199 Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn Leu Trp
200 140 145 150
202 cta gac ggt aaa caa aat aca gta cct ttg gaa acg gtt aaa acg aat 771
203 Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys Thr Asn
204 155 160 165 170
206 aag aaa aat gta act gtt cag gag ttg gat ctt caa gca aga cgt tat 819
207 Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr
208 175 180 185
210 tta cag gaa aaa tat aat tta tat aac tct gat gtt ttt gat ggg aag 867
211 Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys
212 190 195 200
214 gtt cag agg gga tta atc gtg ttt cat act tct aca gaa cct tcg gtt 915
215 Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro Ser Val
216 205 210 215
218 aat tac gat tta ttt ggt gct caa gga cag aat tca aat aca cta tta 963
219 Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln Asn Ser Asn Thr Leu Leu
220 220 225 230
222 aga ata tat aga gat aat aaa acg att aac tct gaa aac atg cat att 1011

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223 Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met His Ile
224 235                240                245                250
226 gat ata tat tta tat aca agt taaacatggt agttttgaac acgtaatggt      1062
227 Asp Ile Tyr Leu Tyr Thr Ser
228                255
230 cagattatta tgaaccgaga ataatctgaa agttttacaag cagtaaaaaa agtatatgtg      1122
232 ctataatatg ctttgagcaa gttggataga tgggtgctat ctgagtataa ggaggtggtg      1182
234 cctatggtgg cattactgaa atcttttagaa aggagacgcc taatgattac aattagtacc      1242
236 aatggttcag tttggtttat tccttattgc attgataggt ctagtaataca agcttattga      1302
238 attaagcaat aaaaaataac catcgctaac tttggctggt ttcgatgggt aaatgggtat      1362
240 taatttaate tttaatctaa aatagccacc gtcttttttaa cggggtcatt agggtaacat      1422
242 gtttgcgcac gttgcccttt t
243                1443
245 (210) SEQ ID NO: 8
246 (211) LENGTH: 257
247 (212) TYPE: PRT
248 (213) ORGANISM: Staphylococcus aureus
250 (400) SEQUENCE: 8
252 Met Lys Lys Thr Ala Phe Ile Leu Leu Leu Phe Ile Ala Leu Thr Trp
253 1                5                10                15
256 Thr Thr Ser Pro Leu Val Asn Gly Ser Glu Lys Ser Glu Glu Ile Asn
257                20                25                30
260 Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Ala Ala Leu Gly
261                35                40                45
264 Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
265                50                55                60
268 Lys Glu Ser His Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly
269 65                70                75                80
272 Phe Phe Thr Asn His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp
273                85                90                95
276 Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr
277                100               105               110
280 Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr
281                115               120               125
284 Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr
285                130               135               140
288 Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
289 145               150               155               160
292 Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val
293                165               170               175
296 Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn
297                180               185               190
300 Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile
301                195               200               205
304 Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
305                210               215               220
308 Ala Gln Gly Gln Asn Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn
309 225               230               235               240
312 Lys Thr Ile Asn Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr
313                245               250               255

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316 Ser
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 1712
322 <212> TYPE: DNA
323 <213> ORGANISM: Staphylococcus aureus
325 <220> FEATURE:
326 <221> NAME/KEY: CDS
327 <222> LOCATION: (244)..(1044)
328 <223> OTHER INFORMATION:
331 <400> SEQUENCE: 9
332 gaactaggta gaaaaataat tatgagaaaa cactatgttg ttaaagatgt ttctgtatat      60
334 aagtttaggt gatgtatagt tacttaattt taaaagcata acttaattaa tataaataac      120
336 atgagattat taaatataat taagtttctt ttaatgtttt tttaattgaa tatttaagat      180
338 tataacatat atttaaagtg tatctagata ctttttggga atgttgata aaggagataa      240
340 aaa atg tat aag aga tta ttt att tca cat gta att ttg ata ttc gca      288
341 Met Tyr Lys Arg Leu Phe Ile Ser His Val Ile Leu Ile Phe Ala
342 1 5 10 15
344 ctg ata tta gtt att tct aca ccc aac gtt tta gca gag agt caa cca      336
345 Leu Ile Leu Val Ile Ser Thr Pro Asn Val Leu Ala Glu Ser Gln Pro
346 20 25 30
348 gat cct aaa cca gat gag ttg cac aaa tcg agt aaa ttc act ggt ttg      384
349 Asp Pro Lys Pro Asp Glu Leu His Lys Ser Ser Lys Phe Thr Gly Leu
350 35 40 45
352 atg gaa aat atg aaa gtt ttg tat gat gat aat cat gta tca gca ata      432
353 Met Glu Asn Met Lys Val Leu Tyr Asp Asp Asn His Val Ser Ala Ile
354 50 55 60
356 aac gtt aaa tct ata gat caa ttt cta tac ttt gac tta ata tat tct      480
357 Asn Val Lys Ser Ile Asp Gln Phe Leu Tyr Phe Asp Leu Ile Tyr Ser
358 65 70 75
360 att aag gac act aag tta ggg aat tat gat aat gtt cga gtc gaa ttt      528
361 Ile Lys Asp Thr Lys Leu Gly Asn Tyr Asp Asn Val Arg Val Glu Phe
362 80 85 90 95
364 aaa aac aaa gat tta gct gat aaa tac aaa gat aaa tac gta gat gtg      576
365 Lys Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys Tyr Val Asp Val
366 100 105 110
368 ttt gga gct aat tat tat tat caa tgt tat ttt tct aaa aaa acg aat      624
369 Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys Tyr Phe Ser Lys Lys Thr Asn
370 115 120 125
372 gat att aat tcg cat caa act gac aaa cga aaa act tgt atg tat ggt      672
373 Asp Ile Asn Ser His Gln Thr Asp Lys Arg Lys Thr Cys Met Tyr Gly
374 130 135 140
376 ggt gta act gag cat aat gga aac caa tta gat aaa tat aga agt att      720
377 Gly Val Thr Glu His Asn Gly Asn Gln Leu Asp Lys Tyr Arg Ser Ile
378 145 150 155
380 act gtt cgg gta ttt gaa gat ggt aaa aat tta tta tct ttt gac gta      768
381 Thr Val Arg Val Phe Glu Asp Gly Lys Asn Leu Leu Ser Phe Asp Val
382 160 165 170 175
384 caa act aat aag aaa aag gtg act gct caa gaa tta gat tac cta act      816
385 Gln Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp Tyr Leu Thr

```

Use of n and x for Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34

L:3931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46

L:5010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53

L:5014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53

L:5037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54

L:22523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:164